

	90	100	110	120	Majority
	L P L L G P I K D R L D Y F Y F Q G - R E E F F R S R I E K Y N S T V F R A N M				
81	L P G I G P I Q D R L D Y F Y N Q G - R E E F F K S R L Q K Y K S T V Y R A N M				AOS-Flax
17	I P F F Q P I K D R L E Y F Y G T G G R D E Y F R S R M Q K Y Q S T V F R A N M				AOS-Guayule
63	L P V G P I K D R W D Y F Y D Q G A - E E F F K S R I R K Y N S T V Y R V N M				AOS-Arabi
77	P P M F G A L K D R H D Y F Y N Q G - R E E Y L K S R M L R Y E S T V Y R T N M				AOS-Melon
43	W P L L G P I S D R L D Y F W F Q G - P E T F F R K R I E K Y K S T V F R A N V				HPL-Guava
27	P P L V G P L K D R L D Y F W F Q G - P E T F F R S R M A T H K S T V F R T N M				HPL-Banana
29	F P L L G P L W D R L D Y N W F Q K - L P D F F S K R V E K Y N S T V F R T N V				HPL-Pepper
22	F P F L G P I K D R Y D Y F Y F Q G - R D E F F R S R I T K Y N S T V F R A N M				HPL-Melon
	P P - - G P F I G S N P R V V V L L D A K S F P V L F D M S K V E K K D L L T I G				Majority
		140	150	160	
120	P P - - G P F I A S N P R V I V L L D A K S F P V L F D M S K V E K K D L F T G				AOS-Flax
57	P P - - G P F V S S N P K W I V L L D A K S F P I L F D V S K V E K K D L F T G				AOS-Guayule
102	P P - - G A F I A E N P Q V V A L L D G K S F P V L F D V D K V E K K D L F T G				AOS-Arabi
116	P P - - G P F I T S D S R V V V L D G K S F P V L F D H S K V E K K D L F T G				AOS-Melon
82	P P C F F S N V N P N V V V V L D C E S F A H L F D M E I V E K S N V L V G				HPL-Guava
66	P P T F F F V G V D P R V V T V L D C T S F S A L F D L E V V E K K N I L I G				HPL-Banana
68	P P C F F F L G V N P N V V A V L D V K S F A H L F D M E I V E K A N V L V G				HPL-Pepper
61	P P - - G P F I S S D S R V V V L L D A L S F P I L F D T A K V E K R N I L D G				HPL-Melon

FIG.1B

	T	Y	M	P	S	T	E	L	T	G	G	Y	R	V	L	S	Y	L	D	P	S	E	P	D	H	A	Q	L	K	N	L	L	F	F	L	L	K	R	S		Majority				
																																						200							
158	T	Y	M	P	S	T	E	L	T	G	G	Y	R	I	L	S	Y	L	D	P	S	E	P	N	H	T	K	L	Q	L	F	N	L	I	K	N	R	R	A	O	S	-	F	lax	
95	T	Y	M	P	S	T	K	L	T	G	A	Y	R	V	L	S	Y	L	D	P	S	E	P	R	H	A	Q	L	K	N	L	F	F	M	K	N	S	S	A	O	S	-	Guayule		
140	T	Y	M	P	S	T	E	L	T	G	G	Y	R	I	L	S	Y	L	D	P	S	E	P	K	H	E	K	L	K	N	L	F	F	L	L	K	S	R	A	O	S	-	Arabi		
154	T	Y	M	P	V	T	E	L	T	G	G	Y	R	V	L	S	Y	I	D	P	S	E	P	D	H	A	K	L	Q	L	I	F	F	L	L	K	H	R	R	A	O	S	-	Melon	
122	D	F	M	P	S	V	K	Y	T	G	N	I	R	V	C	A	Y	L	D	I	S	E	P	H	A	Q	V	K	N	F	A	M	D	I	L	K	R	S	S	H	P	L	-	Guava	
106	D	Y	M	P	S	L	S	F	T	G	D	T	R	V	V	V	Y	L	D	P	S	E	P	D	H	A	R	V	K	S	F	C	L	L	R	R	G	A	A	H	P	L	-	Banana	
108	D	F	M	P	S	V	V	Y	T	G	D	M	R	V	C	A	Y	L	D	I	S	E	P	K	H	T	Q	I	K	N	F	S	L	D	I	L	K	R	S	S	H	P	L	-	Pepper
99	T	Y	M	P	S	L	S	F	T	G	N	I	R	T	C	A	Y	L	D	P	S	E	T	E	H	S	V	L	K	R	L	F	L	S	F	L	A	S	R	H	H	P	L	-	Melon

D R W I P E F X S T L S E L F E T L E S D L A K D G K - A A F N A L - E Q A A F Majority

210 220 230 240

198	D	Y	V	I	P	E	F	S	S	F	T	D	L	C	E	V	V	E	Y	D	L	A	T	K	G	K	-	A	A	F	N	D	P	A	E	Q	A	A	F	A	O	S	-	F	lax
135	N	R	V	I	P	Q	F	E	T	I	Y	T	E	L	F	E	G	L	E	A	E	L	A	K	N	G	K	-	A	A	F	N	D	V	G	E	Q	A	A	F	A	O	S	-	Guayule
180	N	R	I	F	E	F	Q	A	T	Y	S	E	L	F	D	S	L	E	K	E	A	F	L	R	E	-	S	G	F	R	R	F	Q	R	R	N	R	L	A	O	S	-	Arabi		
194	D	K	I	M	P	E	H	S	T	F	S	E	L	F	E	T	L	E	K	D	L	A	A	G	R	-	A	E	Y	N	A	S	G	E	Q	A	A	F	A	O	S	-	Melon		
162	K	V	M	E	S	V	I	S	N	L	D	T	M	W	D	T	I	E	S	L	A	K	D	G	N	A	S	V	I	F	L	-	Q	K	F	L	F	H	P	L	-	Guava			
146	K	T	M	V	S	S	F	L	S	N	L	D	V	M	L	A	T	I	E	Q	I	A	K	D	G	S	A	G	L	F	G	P	L	-	Q	K	C	I	F	H	P	L	-	Banana	
148	K	T	M	V	P	T	L	V	K	E	L	D	T	L	F	G	T	F	E	S	D	L	S	K	S	K	S	A	S	L	P	A	L	-	Q	K	F	L	F	H	P	L	-	Pepper	
139	D	R	F	I	P	L	F	R	S	S	L	S	E	M	F	V	K	L	E	D	K	L	S	E	K	K	I	A	D	F	N	S	I	-	S	D	S	M	S	H	P	L	-	Melon	

FIG.1C

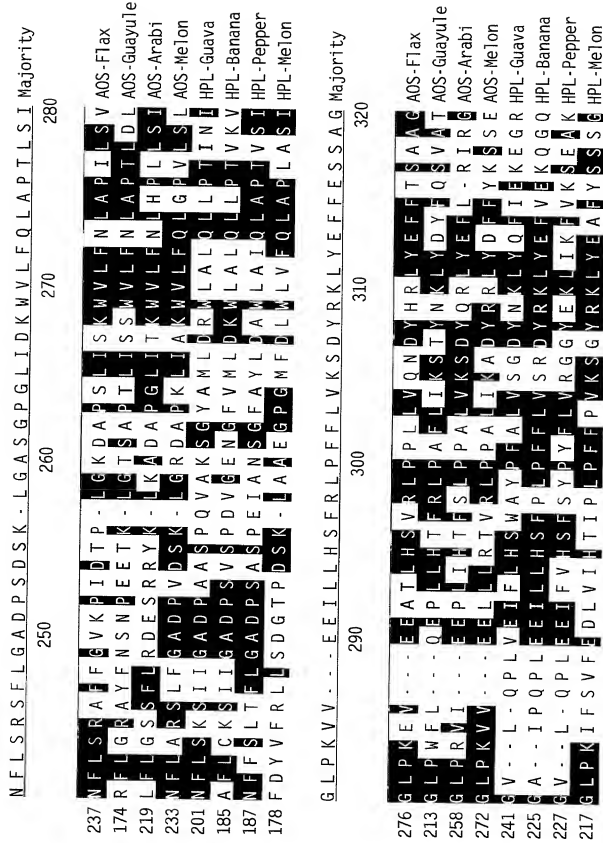


FIG.1D

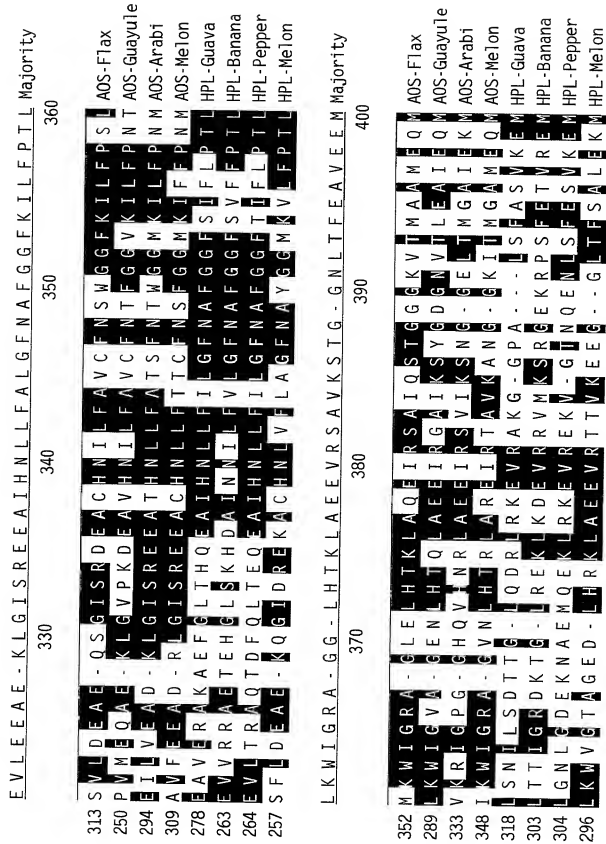
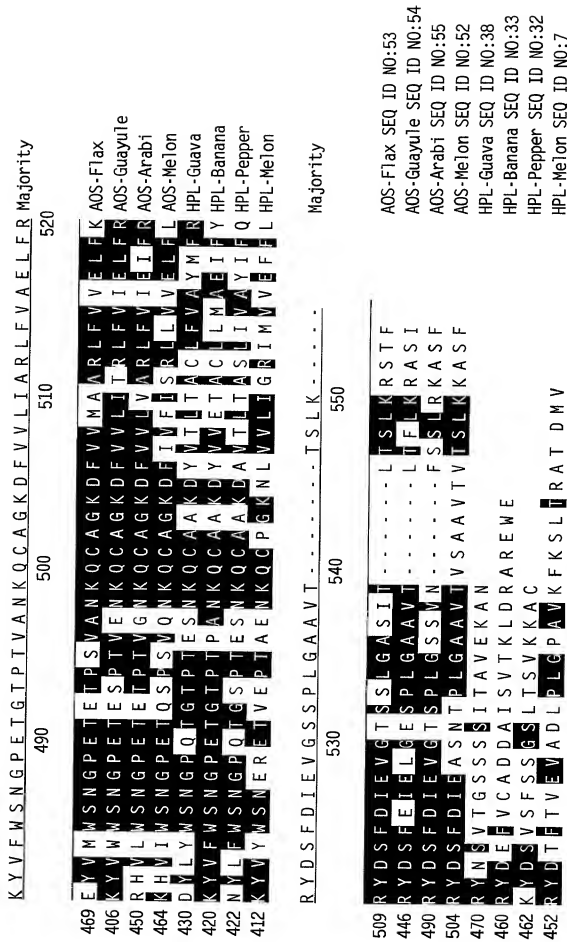


FIG.1E

E L V K S V V Y E A L R I E P P V P L Q Y G R A K K D F V L E S H D A A F E V K Majority														
	410	420	430	440										
391 P	L M K S V V Y E T L R I E P P V A L Q Y G K A K K D F I L E S H E A A Y Q V K AOS-Flax													
328 P	L T K S V V Y E S L R I E P P V P P Q Y G K A K S N F T I E S H D A T F E V K AOS-Guayule													
371 E	L T K S V V Y E C L R F E P P V T A Q Y G R A K K D L V I E S H D A A F K V K AOS-Arabi													
386 P	L M K S V V Y E A L R I E P P V P V Q Y G R A K K D L V V E S H D A A F E I K AOS-Melon													
353 E	L V K S V V Y E T L R L N P P V P F Q Y A R A R K D F Q L K S H D S V F D V K HPL-Guava													
342 E	L V R S T V Y E V L R L N P P V P L Q Y G R A R T D F T L N S H D A A F K V E HPL-Banana													
343 E	L V Q S F V Y E S L R L S P P V P S Q Y A R A R K D F M L S S H D S V Y E I K HPL-Pepper													
333 S	L L K S V V Y E A L R I E P P V P F Q Y G K A K E D I V I Q S H D S S F K I K HPL-Melon													
K G E L L C G Y Q P F A T K D P K V F - D R P E E F V P D R F V G E - G E E L L Majority														
	450	460	470	480										
431 E	G E M L F G Y Q P F A T K D P K I F - D R P E E F V A D R F V G E - G V K L M AOS-Flax													
368 K	G E M L F G Y Q P F A T K D P K V F - D R P E E F V P D R F V G D - G E A L L AOS-Guayule													
411 A	G E M L Y G Y Q P L A T R D P K I F - D R A D E F V P E R F V G E E G E K L L AOS-Arabi													
426 E	G E V I C G Y Q P F A T R D P K I F - D R A D E L V P D R F T G E - G E E L L AOS-Melon													
393 K	G E L L C G Y Q K V V M T D P K V F D E - P E S F N S D R F V Q N S - E L L HPL-Guava													
382 K	G E L L C G Y Q P L V M R D P A V F D D - P E T F A P E R F M - G S G K E L L HPL-Banana													
383 K	G E L L C G Y Q P L V M K D P K V F D E - P E K F M L E R F T K E K G E L L HPL-Pepper													
373 K	G E T I F G Y Q P F A T K D P K I F K D - S E K F V G D R F V G E E G E K L L HPL-Melon													

FIG.1F



Decoration 'Decoration #' : Shade (with solid black) residues that match the Consensus exactly

FIG. 1G

CLONING cDNAs OF AOS AND HPL FROM THE MELON (CANTALOUPE)

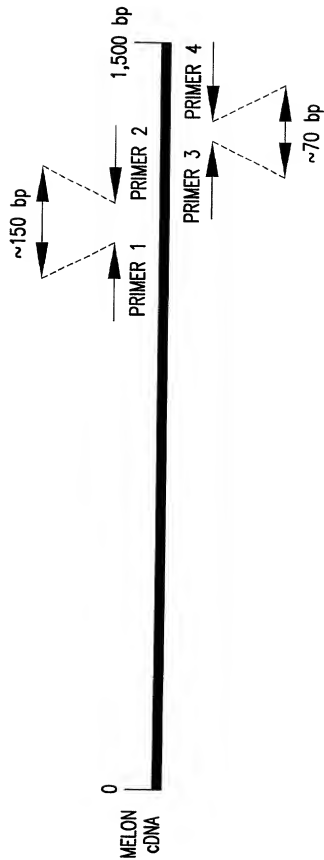


FIG.2A

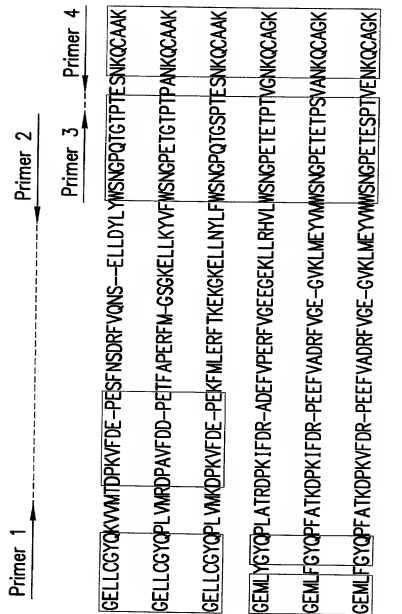


FIG.2B

Sequences of the degenerate primers

Primer 1:

Primer 1A

G E L L C G Y Q SEQ ID NO:22
GGT GAG TTG CTN TGY GGN TAY CA SEQ ID NO:16
(64-fold degenerate)

Primer 1B

G E L L C G Y SEQ ID NO:23
GGT GAG TTG CTN TGY GGN TA SEQ ID NO:17
(32-fold degenerate)

Primer 2:

W S N G P E T SEQ ID NO:24

Antisense of:-

TGG TCN AAY GGN CCR GAG AC SEQ ID NO:18
(64-fold degenerate)

Primer 3:

Y W S N G P E T SEQ ID NO:25
TAC-TGG-TCN-AAY-GGN-CCN SAR AC SEQ ID NO:19
(32-fold degenerate)

Primer 4:

Primer 4A

N K Q C A A X X SEQ ID NO:26

Antisense of:-

AAV AAR CAR TGY GCN GCT AAG GAC SEQ ID NO:20
(64-fold degenerate)

Primer 4B

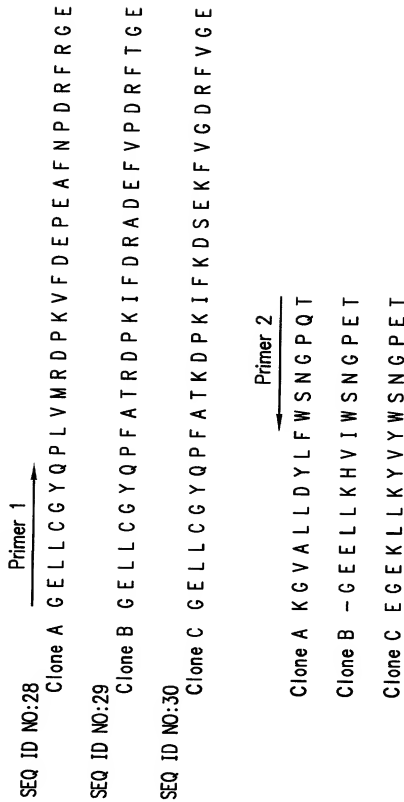
K Q C A A X X SEQ ID NO:27

Antisense of:-

AAR CAR TGY GCN GCT AAG GAC SEQ ID NO:21
(32-fold degenerate)

FIG.3

AMINO ACID SEQUENCE ALIGNMENT OF THE 3 DIFFERENT "150 bp" CLONE



- Typical motif of AOS
- Typical motif of HPL
- Consensus AA

Clone A and clone B: 65% identity
 Clone A and clone C: 57% identity
 Clone B and clone C: 72% identity

FIG.4

% SIMILARITY BETWEEN THE C-TERMINAL
PROTEIN SEQUENCES OF CLONES A, B, C (APPROX 100
AMINO ACIDS) COMPARED TO THE EQUIVALENT REGIONS OF
PUBLISHED 13-HPL OR AOS SEQUENCES

		13-HPL			AOS		
		GUAVA	PEPPER	BANANA	FLAX	GUAYULE	ARABID
MELON	CLONE A	71	69	62	51	50	51
	CLONE B	35	41	43	64	68	66
	CLONE C	32	34	36	51	56	53

FIG.5

PRODUCTS OF 9-HPL FROM 9-HYDROPEROXYLINOLEIC ACID

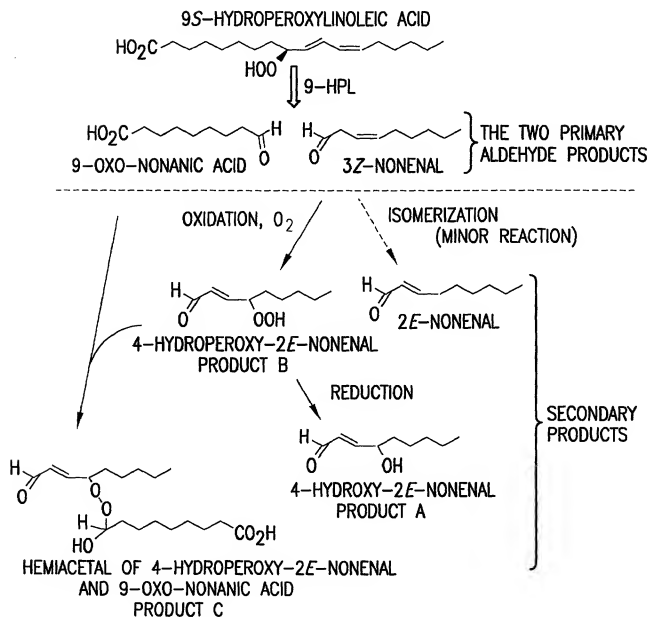


FIG.6